

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,601
Source: IFWP
Date Processed by STIC: 4-6-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/06/2006

PATENT APPLICATION: US/10/573,601

TIME: 10:53:08

Input Set : A:\13301258.APP

Output Set: N:\CRF4\04062006\J573601.raw

3 <110> APPLICANT: HANSSON, HANS-ARNE
 4 JENNISCHE, EVA
 5 LANGE, STEFAN
 6 LON-NROTH, IVAR
 7 ERIKSSON, PETER
 8 PERSSON, ANDERS
 10 <120> TITLE OF INVENTION: NOVEL USE OF ANTISECRETORY FACTOR
 12 <130> FILE REFERENCE: 1003301-000258
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/573,601
 C--> 15 <141> CURRENT FILING DATE: 2006-03-24
 17 <150> PRIOR APPLICATION NUMBER: PCT/SE04/001369
 18 <151> PRIOR FILING DATE: 2004-09-24
 20 <150> PRIOR APPLICATION NUMBER: GB 0322645.3
 21 <151> PRIOR FILING DATE: 2003-09-26
 23 <160> NUMBER OF SEQ ID NOS: 6
 25 <170> SOFTWARE: PatentIn Ver. 3.3
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 382
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 1
 33 Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
 34 1 5 10 15
 36 Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
 37 20 25 30
 39 Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn
 40 35 40 45
 42 Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
 43 50 55 60
 45 Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 46 65 70 75 80
 48 Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
 49 85 90 95
 51 Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
 52 100 105 110
 54 Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala
 55 115 120 125
 57 Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
 58 130 135 140
 60 Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
 61 145 150 155 160
 63 Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
 64 165 170 175

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```

66 Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
67           180           185           190
69 Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
70           195           200           205
72 Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
73           210           215           220
75 Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
76 225           230           235           240
78 Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
79           245           250           255
81 Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
82           260           265           270
84 Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala Tyr
85           275           280           285
87 Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
88           290           295           300
90 Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
91 305           310           315           320
93 Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
94           325           330           335
96 Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
97           340           345           350
99 Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg
100          355           360           365
102 Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
103          370           375           380
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 1323
108 <212> TYPE: DNA
109 <213> ORGANISM: Homo sapiens
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (63)..(1208)
115 <400> SEQUENCE: 2
116 aattggagga gttgttgta ggccgtcccg gagaccggt cgggaggag gaaggtggca 60
118 ag atg gtg ttg gaa agc act atg gtg tgt gtg gac aac agt gag tat 107
119 Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
120 1 5 10 15
122 atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat 155
123 Met Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp
124 20 25 30
126 gct gtc aac ata gtt tgt cat tca aag acc cgc agc aac cct gag aac 203
127 Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn
128 35 40 45
130 aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca 251
131 Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr
132 50 55 60
134 ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa 299
135 Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln

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136	65	70	75	
138	ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtg gcc cat ctg	347		
139	Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu			
140	80 85 90 95			
142	gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc	395		
143	Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala			
144	100 105 110			
146	ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg	443		
147	Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu			
148	115 120 125			
150	gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt	491		
151	Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe			
152	130 135 140			
154	ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg	539		
155	Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr			
156	145 150 155			
158	ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct	587		
159	Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro			
160	160 165 170 175			
162	ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt	635		
163	Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly			
164	180 185 190			
166	gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga	683		
167	Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly			
168	195 200 205			
170	gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct	731		
171	Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser			
172	210 215 220			
174	atg gaa gag cag cgg cac gca gga gga gga gcg cgg cgg gca gct cga	779		
175	Met Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg			
176	225 230 235			
178	gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca	827		
179	Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser			
180	240 245 250 255			
182	gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc	875		
183	Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg			
184	260 265 270			
186	act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct	923		
187	Thr Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala			
188	275 280 285			
190	tat gcc atg cag atg tcc ctg cag gga gca gag ttt ggc cag gcg gaa	971		
191	Tyr Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu			
192	290 295 300			
194	tca gca gac att gat gcc agc tca gct atg gac aca tct gag cca gcc	1019		
195	Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala			
196	305 310 315			
198	aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag	1067		
199	Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln			
200	320 325 330 335			

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```

202 agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att 1115
203 Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile
204          340          345          350
206 cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga 1163
207 Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
208          355          360          365
210 agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg 1208
211 Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
212          370          375          380
214 tagctgagtc tgcttagggg actgggaagc acggaatata ggggtagatg tggttatctg 1268
216 taaccattac agcctaaata aagcttgcca acttttaaaa aaaaaaaaaa aaaaa 1323
219 <210> SEQ ID NO: 3
220 <211> LENGTH: 46
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
226 amino acid sequence
228 <220> FEATURE:
229 <221> NAME/KEY: MOD_RES
230 <222> LOCATION: (1)..(35)
231 <223> OTHER INFORMATION: This region may or may not be present
233 <220> FEATURE:
234 <221> NAME/KEY: MOD_RES
235 <222> LOCATION: (38)
236 <223> OTHER INFORMATION: His, Arg or Lys
238 <220> FEATURE:
239 <221> NAME/KEY: MOD_RES
240 <222> LOCATION: (39)
241 <223> OTHER INFORMATION: Ser or Leu
243 <220> FEATURE:
244 <221> NAME/KEY: MOD_RES
245 <222> LOCATION: (41)
246 <223> OTHER INFORMATION: Thr or Ala
248 <220> FEATURE:
249 <221> NAME/KEY: MOD_RES
250 <222> LOCATION: (43)..(46)
251 <223> OTHER INFORMATION: This region may or may not be present
253 <400> SEQUENCE: 3
254 Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
255 1          5          10          15
257 Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
258          20          25          30
W--> 260 Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu
261          35          40          45
264 <210> SEQ ID NO: 4
265 <211> LENGTH: 51
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence

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Input Set : A:\13301258.APP

Output Set: N:\CRF4\04062006\J573601.raw

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269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
271     amino acid sequence
273 <220> FEATURE:
274 <221> NAME/KEY: MOD_RES
275 <222> LOCATION: (1)..(35)
276 <223> OTHER INFORMATION: This region may or may not be present
278 <220> FEATURE:
279 <221> NAME/KEY: MOD_RES
280 <222> LOCATION: (38)
281 <223> OTHER INFORMATION: His, Arg or Lys
283 <220> FEATURE:
284 <221> NAME/KEY: MOD_RES
285 <222> LOCATION: (39)
286 <223> OTHER INFORMATION: Ser or Leu
288 <220> FEATURE:
289 <221> NAME/KEY: MOD_RES
290 <222> LOCATION: (41)
291 <223> OTHER INFORMATION: Thr or Ala
293 <220> FEATURE:
294 <221> NAME/KEY: MOD_RES
295 <222> LOCATION: (43)..(51)
296 <223> OTHER INFORMATION: This region may or may not be present
298 <400> SEQUENCE: 4
299 Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met
300   1             5             10             15
302 Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala
303   20             25             30
W--> 305 Val Asn Ile Val Cys Xaa Xaa Lys Xaa Arg Ser Asn Pro Glu Asn Asn
306   35             40             45
308 Val Gly Leu
309   50
312 <210> SEQ ID NO: 5
313 <211> LENGTH: 80
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
319     amino acid sequence
321 <220> FEATURE:
322 <221> NAME/KEY: MOD_RES
323 <222> LOCATION: (1)..(35)
324 <223> OTHER INFORMATION: This region may or may not be present
326 <220> FEATURE:
327 <221> NAME/KEY: MOD_RES
328 <222> LOCATION: (38)
329 <223> OTHER INFORMATION: His, Arg or Lys
331 <220> FEATURE:
332 <221> NAME/KEY: MOD_RES

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/573,601

DATE: 04/06/2006
TIME: 10:53:09

Input Set : A:\13301258.APP
Output Set: N:\CRF4\04062006\J573601.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 38,39,41 ✓

Seq#:4; Xaa Pos. 38,39,41 ✓

Seq#:5; Xaa Pos. 38,39,41 ✓

Seq#:6; Xaa Pos. 38,39,41 ✓

VERIFICATION SUMMARY

DATE: 04/06/2006

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Input Set : A:\13301258.APP

Output Set: N:\CRF4\04062006\J573601.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:32
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:32
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:32
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:32